

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/784,358

DATE: 07/30/2001

TIME: 15:10:33

Input Set : A:\LFX-0134-USA SEQLIST.txt

Output Set: N:\CRF3\07302001\I784358.raw

4 <110> APPLICANT: Donoho, Gregory
 5 Scoville, John
 6 Turner, C. Alexander Jr.
 7 Friedrich, Glenn
 8 Zambrowicz, Brian
 9 Sands, Arthur T.
 11 <120> TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
 12 POLYNUCLEOTIDES ENCODING THE SAME
 14 <130> FILE REFERENCE: LEX-0134-USA
 16 <140> CURRENT APPLICATION NUMBER: US/09/784,358
 16 <141> CURRENT FILING DATE: 2001-02-15
 16 <150> PRIOR APPLICATION NUMBER: US 60/183,282
 17 <151> PRIOR FILING DATE: 2000-02-17
 19 <160> NUMBER OF SEQ ID NOS: 17
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5076
 25 <212> TYPE: DNA
 26 <213> ORGANISM: homo sapiens
 28 <400> SEQUENCE: 1
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 31 tctctctcagg gaagttttct ggaagacaca acaggggagc agttctctac ttatcgctat 180
 32 gatgaccaga cctcaagaaa cactcgttca gatgaagaca aagatggcaa ctgggatgct 240
 33 tggggggagc ggagtgaact ctcccggacc tgtgggggag gagcctcata ttctctgagg 300
 34 agatgtttga ctggaaggaa ttgtgaaggc cagaacatc ggtacaagac atgcagcaat 360
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 37 tgtgcaactca agtgcctatc acaaggacaa aacttgggtg tggagctggc acctaaagga 540
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 40 gccggggatg gctccacctg caggcttgta cggggacaat caaagtccaa cgtttctctt 720
 41 gaaaaaagag aagaaaatgt aattgctgtt cctttgggaa gtggaagtgt gagaattaca 780
 42 gtgaaaggac ctgcccacct ctttattgaa tcaaaaacac ttcaagggaag caaaggagaa 840
 43 cacagcttta acagccccgg cgtctttgtc gtgaaaaaca caacagtga atttcagagg 900
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ENTERED

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57	ataacaaac	aaajaaccaac	gttcattcca	gaacccctgt	cagccctgaa	taacacgtgt	1740
58	ggccacagtg	tgcaggctcc	cgagggtgaag	tgcctgtgtg	tcctcacatt	cacgcagact	1800
59	gagactgagc	tgcacagaga	agagtgtgaa	ggcccaagc	tgcacacaga	acggccctgc	1860
60	ctcctggaag	catgtgatga	gagcccgcc	tcocgagagc	taacacatcc	tcctcctgag	1920
61	gacagtgaga	cgacttaaga	ctgggagtag	gctgggttca	cccttgcac	agcaacatgc	1980
62	ttgggaggcc	atcaagaagc	catagcagtg	tgtttacata	tcacagacca	gcagacagtc	2040
63	aattgacagc	tgtgtgatat	ggtccacccg	ccctcagcca	tgagccaggc	ctgtaacaca	2100
64	gagccctgtc	cccccagggt	gcattgtggc	tcttggtggc	ccctgtccagc	taacctgtga	2160
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77	atccccaagt	caggctcact	aaaaatccac	ggcttctgtg	cccccagcat	cggcgtgtac	2940
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102	agtgaaggcc	tgtgtgatca	cctccagaag	ccactggctg	ggtttgagcc	ctgtaacatc	4440
103	cgggactgcc	cagcgagggt	gttcacaagt	gtgtggtcac	agtgtctctg	gtcttgcggg	4500
104	gaaggatacc	acagtcggca	ggtgacgtgc	aagcggacaa	aagccaatgg	aactgtjcag	4560

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105 gtggtgtctc caagagcatg tgcctctaaa gaccggcctc tgggaagaaa accatgtttt 4620
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107 gctgtgagga tgcagcagcg tccacacagc tctcaacaca acagctctga ctccaactgt 4740
108 gatgacagaa agagaccacac ctttaagaagg aactgcacat caggggcctg tgatgtgtgt 4800
109 tggcacacag gcccttggaa gccctgtaca gcagcctgtg gcagggttt ccagtctcgg 4860
110 aaagtgcact gtatccacac aaggagttgc aaacctgtgg ccaagagaca ctgtgtacag 4920
111 aaaaagaaac caatttctct ggggcactgt cttgggccc cctgtgatag agactgcaca 4980
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119 <212> TYPE: PR1
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122 <400> SEQUENCE: 2
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126 20 25 30
127 Tyr Phe Leu Pro Glu Phe Ala Leu Ser Pro Gln Gly Ser Phe Leu Glu
128 35 40 45
129 Asp Thr Thr Gly Glu Gln Phe Leu Thr Tyr Arg Tyr Asp Asp Gln Thr
130 50 55 60
131 Ser Arg Asn Thr Arg Ser Asp Glu Asp Lys Asp Gly Asn Trp Asp Ala
132 65 70 75 80
133 Trp Gly Asp Trp Ser Asp Cys Ser Arg Thr Cys Gly Gly Gly Ala Ser
134 85 90 95
135 Tyr Ser Leu Arg Arg Cys Leu Thr Gly Arg Asn Cys Glu Gly Gln Asn
136 100 105 110
137 Ile Arg Tyr Lys Thr Cys Ser Asn His Asp Cys Pro Pro Asp Ala Glu
138 115 120 125
139 Asp Phe Arg Ala Gln Gln Cys Ser Ala Tyr Asn Asp Val Gln Tyr Gln
140 130 135 140
141 Gly His Tyr Tyr Glu Trp Leu Pro Arg Tyr Asn Asp Pro Ala Ala Pro
142 145 150 155 160
143 Cys Ala Leu Lys Cys His Ala Gln Gly Gln Asn Leu Val Val Glu Leu
144 165 170 175
145 Ala Pro Lys Val Leu Asp Gly Thr Arg Cys Asn Thr Asp Ser Leu Asp
146 180 185 190
147 Met Cys Ile Ser Gly Ile Cys Gln Ala Val Gly Cys Asp Arg Gln Leu
148 195 200 205
149 Gly Ser Asn Ala Lys Glu Asp Asn Cys Gly Val Cys Ala Gly Asp Gly
150 210 215 220
151 Ser Thr Cys Arg Leu Val Arg Gly Gln Ser Lys Ser His Val Ser Pro
152 225 230 235 240
153 Glu Lys Arg Glu Glu Asn Val Ile Ala Val Pro Leu Gly Ser Arg Ser
154 245 250 255
155 Val Arg Ile Thr Val Lys Gly Pro Ala His Leu Phe Ile Glu Ser Lys
156 260 265 270
157 Thr Leu Gln Gly Ser Lys Gly Glu His Ser Phe Asn Ser Pro Gly Val

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158          275          280          285
159 Phe Val Val Glu Asn Thr Thr Val Glu Phe Gln Arg Gly Ser Glu Arg
160          290          295          300
161 Gln Thr Phe Lys Ile Pro Gly Pro Leu Met Ala Asp Phe Ile Phe Lys
162 305          310          315          320
163 Thr Arg Tyr Thr Ala Ala Lys Asp Ser Val Val Gln Phe Phe Phe Tyr
164          325          330          335
165 Gln Pro Ile Ser His Gln Trp Arg Gln Thr Asp Phe Phe Pro Cys Thr
166          340          345          350
167 Val Thr Cys Gly Gly Gly Tyr Gln Leu Asn Ser Ala Glu Cys Val Asp
168          355          360          365
169 Ile Arg Leu Lys Arg Val Val Pro Asp His Tyr Cys His Tyr Tyr Pro
170          370          375          380
171 Glu Asn Val Lys Pro Lys Pro Lys Leu Lys Glu Cys Ser Met Asp Pro
172 385          390          395          400
173 Cys Pro Ser Ser Asp Gly Phe Lys Glu Ile Met Pro Tyr Asp His Phe
174          405          410          415
175 Gln Pro Leu Pro Arg Trp Glu His Asn Pro Trp Thr Ala Cys Ser Val
176          420          425          430
177 Ser Cys Gly Gly Gly Ile Gln Arg Arg Ser Phe Val Cys Val Glu Glu
178          435          440          445
179 Ser Met His Gly Glu Ile Leu Gln Val Glu Glu Trp Lys Cys Met Tyr
180          450          455          460
181 Ala Pro Lys Pro Lys Val Met Gln Thr Cys Asn Leu Phe Asp Cys Pro
182 465          470          475          480
183 Lys Trp Ile Ala Met Glu Trp Ser Gln Cys Thr Val Thr Cys Gly Arg
184          485          490          495
185 Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asn His Arg Gly Glu His
186          500          505          510
187 Val Gly Gly Cys Asn Pro Gln Leu Lys Leu His Ile Lys Glu Glu Cys
188          515          520          525
189 Val Ile Pro Ile Pro Cys Tyr Lys Pro Lys Glu Lys Ser Pro Val Glu
190          530          535          540
191 Ala Lys Leu Pro Trp Leu Lys Gln Ala Gln Glu Leu Glu Glu Thr Arg
192 545          550          555          560
193 Ile Ala Thr Glu Glu Pro Thr Phe Ile Pro Glu Pro Trp Ser Ala Cys
194          565          570          575
195 Ser Thr Thr Cys Gly Pro Gly Val Gln Val Arg Glu Val Lys Cys Arg
196          580          585          590
197 Val Leu Leu Thr Phe Thr Gln Thr Glu Thr Glu Leu Pro Glu Glu Glu
198          595          600          605
199 Cys Glu Gly Pro Lys Leu Pro Thr Glu Arg Pro Cys Leu Leu Glu Ala
200          610          615          620
201 Cys Asp Glu Ser Pro Ala Ser Arg Glu Leu Asp Ile Pro Leu Pro Glu
202 625          630          635          640
203 Asp Ser Glu Thr Thr Tyr Asp Trp Glu Tyr Ala Gly Phe Thr Pro Cys
204          645          650          655
205 Thr Ala Thr Cys Leu Gly Gly His Gln Glu Ala Ile Ala Val Cys Leu
206          660          665          670

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207 His Ile Gln Thr Gln Gln Thr Val Asn Asp Ser Leu Cys Asp Met Val
208          675          680          685
209 His Arg Pro Pro Ala Met Ser Gln Ala Cys Asn Thr Glu Pro Cys Pro
210          690          695          700
211 Pro Arg Trp His Val Gly Ser Trp Gly Pro Cys Ser Ala Thr Cys Gly
212 705          710          715          720
213 Val Gly Ile Gln Thr Arg Asp Val Tyr Cys Leu His Pro Gly Glu Thr
214          725          730          735
215 Pro Ala Pro Pro Glu Glu Cys Arg Asp Glu Lys Pro His Ala Leu Gln
216          740          745          750
217 Ala Cys Asn Gln Phe Asp Cys Pro Pro Gly Trp His Ile Glu Glu Trp
218          755          760          765
219 Gln Gln Cys Ser Arg Thr Cys Gly Gly Gly Thr Gln Asn Arg Arg Val
220          770          775          780
221 Thr Cys Arg Gln Leu Leu Thr Asp Gly Ser Phe Leu Asn Leu Ser Asp
222 785          790          795          800
223 Glu Leu Cys Gln Gly Pro Lys Ala Ser Ser His Lys Ser Cys Ala Arg
224          805          810          815
225 Thr Asp Cys Pro Pro His Leu Ala Val Gly Asp Trp Ser Lys Cys Ser
226          820          825          830
227 Val Ser Cys Gly Val Gly Ile Gln Arg Arg Lys Gln Val Cys Gln Arg
228          835          840          845
229 Leu Ala Ala Lys Gly Arg Arg Ile Pro Leu Ser Glu Met Met Cys Arg
230          850          855          860
231 Asp Leu Pro Gly Phe Pro Leu Val Arg Ser Cys Gln Met Pro Glu Cys
232 865          870          875          880
233 Ser Lys Ile Lys Ser Glu Met Lys Thr Lys Leu Gly Glu Gln Gly Pro
234          885          890          895
235 Gln Ile Leu Ser Val Gln Arg Val Tyr Ile Gln Thr Arg Glu Glu Lys
236          900          905          910
237 Arg Ile Asn Leu Thr Ile Gly Ser Arg Ala Tyr Leu Leu Pro Asn Thr
238          915          920          925
239 Ser Val Ile Ile Lys Cys Pro Val Arg Arg Phe Gln Lys Ser Leu Ile
240          930          935          940
241 Gln Trp Glu Lys Asp Gly Arg Cys Leu Gln Asn Ser Lys Arg Leu Gly
242 945          950          955          960
243 Ile Thr Lys Ser Gly Ser Leu Lys Ile His Gly Leu Ala Ala Pro Asp
244          965          970          975
245 Ile Gly Val Tyr Arg Cys Ile Ala Gly Ser Ala Gln Glu Thr Val Val
246          980          985          990
247 Leu Lys Leu Ile Gly Thr Asp Asn Arg Leu Ile Ala Arg Pro Ala Leu
248          995          1000          1005
249 Arg Glu Pro Met Arg Glu Tyr Pro Gly Met Asp His Ser Glu Ala Asn
250          1010          1015          1020
251 Ser Leu Gly Val Thr Trp His Lys Met Arg Gln Met Trp Asn Asn Lys
252 1025          1030          1035          1040
253 Asn Asp Leu Tyr Leu Asp Asp Asp His Ile Ser Asn Gln Pro Phe Leu
254          1045          1050          1055
255 Arg Ala Leu Leu Gly His Cys Ser Asn Ser Ala Gly Ser Thr Asn Ser

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs. Replaced Current Application No

L:16 M:271 C: Current Filing Date differs. Replaced Current Filing Date